

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings of claims in the application:

**Listing of Claims:**

1. (currently amended) A method for analyzing gene expression comprising:
  - obtaining expression levels of ~~a plurality of~~ genes;
  - selecting at least one biological characteristic from a plurality of biological characteristics stored in a database; wherein the biological characteristics comprise genomic information about the genes, structural information about ~~[[the]]~~ products of the genes~~[[;]]~~, and biological functions of the genes; wherein the biological characteristics are described using a gene ontology system; wherein the database includes database entities being designed to mimic biological entities, a first relationship among the database entities mimicking a second relationship among biological macromolecules; and
  - ~~analyzing the expression levels according to the selected at least one biological characteristic~~grouping the expression levels according to the selected at least one biological characteristic;
  - performing one or more statistical methods to the grouped expression levels.
- 2.-6. (canceled)
7. (original) The method of Claim 1 wherein the plurality of biological characteristics comprise orthologous genes.
- 8.-12. (canceled)
13. (original) The method of Claim 1 wherein the database is a relational database.

14. (original) The method of Claim 1 wherein the database is an object oriented database.

15. (currently amended) The method of Claim 13 wherein the plurality of biological characteristics are ~~retrived~~retrieved using SQL (Structured Query Language) statements.

16.-45. (canceled).

46. (new) A method for analyzing gene expression comprising:  
obtaining expression levels of genes;

selecting at least one biological characteristic from a plurality of biological characteristics stored in a database; wherein the biological characteristics comprise genomic information about the genes, structural information about products of the genes, and biological functions of the genes; wherein the biological characteristics are described using a gene ontology system; wherein the database includes database entities being designed to mimic biological entities, a first relationship among the database entities mimicking a second relationship among biological macromolecules;

selecting certain expression levels for cluster analysis according to the selected at least one biological characteristic;

clustering according to the selected at least one biological characteristic.

47. (new) The method of Claim 46 wherein the clustering process comprises multiple dimensional clustering according to the selected biological characteristics.

48. (new) The method of Claim 47, and further comprising data mining.

49. (new) The method of Claim 46 wherein the plurality of biological characteristics comprise orthologous genes.

50. (new) The method of Claim 46 wherein the database is a relational database.

51. (new) The method of Claim 46 wherein the database is an object oriented database.